

Group 1814

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OK 184 RUGAISKY

SEQUENCE LISTING

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4 (1) GENERAL INFORMATION:

5

6 (i) APPLICANT: WALLACH, DAVID
7 NOPHAR, YARON
8 KEMPER, OLIVER
9 ENGELMANN, HARTMUT
10 BRAKEBUSCH, CORD
11 ADERKA, DAN

12

13 (ii) TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR
14 NECROSIS FACTOR BINDING PROTEIN I (TBP-I)

15

16 (iii) NUMBER OF SEQUENCES: 26

17

18 (iv) CORRESPONDENCE ADDRESS:

19 (A) ADDRESSEE: Browdy and Neimark
20 (B) STREET: 419 Seventh Street, N.W., Suite 300
21 (C) CITY: Washington
22 (D) STATE: DC
23 (E) COUNTRY: USA
24 (F) ZIP: 20004

25

26 (v) COMPUTER READABLE FORM:

27 (A) MEDIUM TYPE: Floppy disk
28 (B) COMPUTER: IBM PC compatible
29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

31

32 (vi) CURRENT APPLICATION DATA:

33 (A) APPLICATION NUMBER: US 07/625668
34 (B) FILING DATE: 13-DEC-1990
35 (C) CLASSIFICATION:

36

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: BROWDY, ROGER L
39 (B) REGISTRATION NUMBER: 25,618
40 (C) REFERENCE/DOCKET NUMBER: WALLACH4

41

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: 202-628-5197
44 (B) TELEFAX: 202-737-3528
45 (C) TELEX: 248633

46

47

48 (2) INFORMATION FOR SEQ ID NO:1:

49

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 2175 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: single

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54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: cDNA
57
58
59 (ix) FEATURE:
60 (A) NAME/KEY: CDS
61 (B) LOCATION: 256..1620
62
63 (ix) FEATURE:
64 (A) NAME/KEY: mat_peptide
65 (B) LOCATION: 319..1620
66
67
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70 CGGCCAGTG ATCTTGAACC CCAAAGGCCA GAACTGGAGC CTCAGTCCAG AGAATTCTGA 60
71
72 GAAAATTAAA GCAGAGAGGA GGGGAGAGAT CACTGGGACC AGGCCGTGAT CTCTATGCC 120
73
74 GAGTCTCAAC CCTCAACTGT CACCCCAAGG CACTTGGGAC GTCCTGGACA GACCGAGTCC 180
75
76 CGGGAAGCCC CAGCACTGCC GCTGCCACAC TGCCCTGAGC CCAAATGGGG GAGTGAGAGG 240
77
78 CCATAGCTGT CTGGC ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCG 291
79 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro
80 -21 -20 -15 -10 -10
81
82 CTG GTG CTC CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT 339
83 Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile
84 -5 1 5
85
86 GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT 387
87 Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys
88 10 15 20
89
90 CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC 435
91 Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
92 25 30 35
93
94 AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG 483
95 Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly
96 40 45 50 55
97
98 CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA 531
99 Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser
100 60 65 70
101
102 GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC CGA AAG GAA 579
103 Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu
104 75 80 85
105
106 ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC CGG GAC ACC GTG 627

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107 Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val
108 90 95 100
109
110 TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT 675
111 Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu
112 105 110 115
113
114 TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC 723
115 Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu
116 120 125 130 135
117
118 TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC 771
119 Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe
120 140 145 150
121
122 TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT AAC TGT AAG AAA AGC 819
123 Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser
124 155 160 165
125
126 CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG AAT GTT AAG GGC 867
127 Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly
128 170 175 180
129
130 ACT GAG GAC TCA GGC ACC ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT 915
131 Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe
132 185 190 195
133
134 GGT CTT TGC CTT TTA TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC 963
135 Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr
136 200 205 210 215
137
138 CAA CGG TGG AAG TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA 1011
139 Gln Arg Trp Lys Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr
140 220 225 230
141
142 CCT GAA AAA GAG GGG GAG CTT GAA GGA ACT ACT ACT AAG CCC CTG GCC 1059
143 Pro Glu Lys Glu Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala
144 235 240 245
145
146 CCA AAC CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC CCC ACC CTG GGC 1107
147 Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly
148 250 255 260
149
150 TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC 1155
151 Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
152 265 270 275
153
154 CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA 1203
155 Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro
156 280 285 290 295
157
158 CCC TAT CAG GGG GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC TCC GAC 1251
159 Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp

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160	300	305	310	
161				
162	CCC ATC CCC AAC CCC CTT CAG AAG TGG GAG GAC AGC GCC CAC AAG CCA			1299
163	Pro Ile Pro Asn Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro			
164	315	320	325	
165				
166	CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC GCC GTG GTG GAG			1347
167	Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu			
168	330	335	340	
169				
170	AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG			1395
171	Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu			
172	345	350	355	
173				
174	AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG			1443
175	Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu			
176	360	365	370	375
177				
178	CGC GAG GCG CAA TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG			1491
179	Arg Glu Ala Gln Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro			
180	380	385	390	
181				
182	CGG CGC GAG GCC ACG CTG GAG CTG CTG GGA CGC GTG CTC CGC GAC ATG			1539
183	Arg Arg Glu Ala Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met			
184	395	400	405	
185				
186	GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG CTT TGC GGC CCC			1587
187	Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro			
188	410	415	420	
189				
190	GCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGAGGCTGCG CCCTGCAGGC			1640
191	Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg			
192	425	430		
193				
194	AGCTCTAAGG ACCGTCTGC GAGATCGCCT TCCAACCCCA CTTTTTCTG GAAAGGAGGG			1700
195				
196	GTCCTGCAGG GGCAAGCAGG AGCTAGCAGC CGCCTACTTG GTGCTAACCC CTCGATGTAC			1760
197				
198	ATAGCTTTTC TCAGCTGCCT GCGCGCCGCC GACAGTCAGC GCTGTGCGCG CGGAGAGAGG			1820
199				
200	TGCGCCGTGG GCTCAAGAGC CTGAGTGGGT GGTTGCGAG GATGAGGGAC GCTATGCCTC			1880
201				
202	ATGCCCGTTT TGGGTGTCCT CACCAAGCAAG GCTGCTCGGG GGCCCTGGT TCGTCCCTGA			1940
203				
204	GCCTTTTCA CAGTGCATAA GCAGTTTTT TTGTTTTGT TTTGTTTTGT TTTGTTTTA			2000
205				
206	AATCAATCAT GTTACACTAA TAGAAACTTG GCACTCCTGT GCCCTCTGCC TGGACAAGCA			2060
207				
208	CATAGCAAGC TGAACGTGCC TAAGGCAGGG GCGAGCACGG AACAAATGGGG CCTTCAGCTG			2120
209				
210	GAGCTGTGGA CTTTTGTACA TACACTAAAA TTCTGAAGTT AAAAAAAA AAAAA			2175
211				
212				

213 (2) INFORMATION FOR SEQ ID NO:2:

214

215 (i) SEQUENCE CHARACTERISTICS:

216 (A) LENGTH: 455 amino acids
217 (B) TYPE: amino acid
218 (D) TOPOLOGY: linear

219

220 (ii) MOLECULE TYPE: protein

221

222 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

223

224 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
225 -21 -20 -15 -10

226

227 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
228 -5 1 5 10

229

230 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
231 15 20 25

232

233 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
234 30 35 40

235

236 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
237 45 50 55

238

239 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
240 60 65 70 75

241

242 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
243 80 85 90

244

245 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
246 95 100 105

247

248 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
249 110 115 120

250

251 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
252 125 130 135

253

254 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
255 140 145 150 155

256

257 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
258 160 165 170

259

260 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
261 175 180 185

262

263 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
264 190 195 200

265

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266 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
267 205 210 215
268
269 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
270 220 225 230 235
271
272 Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
273 240 245 250
274
275 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
276 255 260 265
277
278 Pro Ser Ser Thr Phe Thr Ser Ser Thr Tyr Thr Pro Gly Asp Cys
279 270 275 280
280
281 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
282 285 290 295
283
284 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
285 300 305 310 315
286
287 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
288 320 325 330
289
290 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
291 335 340 345
292
293 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
294 350 355 360
295
296 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
297 365 370 375
298
299 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
300 380 385 390 395
301
302 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
303 400 405 410
304
305 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
306 415 420 425
307
308 Pro Ala Pro Ser Leu Leu Arg
309 430
310
311 (2) INFORMATION FOR SEQ ID NO:3:
312
313 (i) SEQUENCE CHARACTERISTICS:
314 (A) LENGTH: 26 base pairs
315 (B) TYPE: nucleic acid
316 (C) STRANDEDNESS: single
317 (D) TOPOLOGY: linear
318

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319 (ii) MOLECULE TYPE: protein

320

321

322

323 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

324

325 GGNNGTYCCNT TYATRTARGT DGGNGT

26

326

327 (2) INFORMATION FOR SEQ ID NO:4:

328

329 (i) SEQUENCE CHARACTERISTICS:

330 (A) LENGTH: 17 base pairs
331 (B) TYPE: nucleic acid
332 (C) STRANDEDNESS: single
333 (D) TOPOLOGY: linear

334

335 (ii) MOLECULE TYPE: cDNA

336

337

338

339 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

340

341 GGNNGTYCCNT TYATRTA

17

342

343 (2) INFORMATION FOR SEQ ID NO:5:

344

345 (i) SEQUENCE CHARACTERISTICS:
346 (A) LENGTH: 17 base pairs
347 (B) TYPE: nucleic acid
348 (C) STRANDEDNESS: single
349 (D) TOPOLOGY: linear

350

351 (ii) MOLECULE TYPE: cDNA

352

353 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

354

355 TTYATRTARG TDGGNGT

17

356

357 (2) INFORMATION FOR SEQ ID NO:6:

358

359 (i) SEQUENCE CHARACTERISTICS:
360 (A) LENGTH: 27 base pairs
361 (B) TYPE: nucleic acid
362 (C) STRANDEDNESS: single
363 (D) TOPOLOGY: linear

364

365 (ii) MOLECULE TYPE: cDNA

366

367

368

369 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

370

371 CGGCCGATGG GCCTCTCCAC CGTGCCT

27

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372
373 (2) INFORMATION FOR SEQ ID NO:7:
374
375 (i) SEQUENCE CHARACTERISTICS:
376 (A) LENGTH: 27 base pairs
377 (B) TYPE: nucleic acid
378 (C) STRANDEDNESS: single
379 (D) TOPOLOGY: linear
380

381 (ii) MOLECULE TYPE: cDNA
382
383
384

385 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
386

387 AATAGTATTT CTAATCTGGG GTAGGCA

27

389 (2) INFORMATION FOR SEQ ID NO:8:
390

391 (i) SEQUENCE CHARACTERISTICS:
392 (A) LENGTH: 6 amino acids
393 (B) TYPE: amino acid
394 (C) STRANDEDNESS: single
395 (D) TOPOLOGY: linear
396

397 (ii) MOLECULE TYPE: peptide
398

399 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
400

401 Met Asp Ser Val Cys Pro

402 1 5

404 (2) INFORMATION FOR SEQ ID NO:9:
405

406 (i) SEQUENCE CHARACTERISTICS:
407 (A) LENGTH: 23 base pairs
408 (B) TYPE: nucleic acid
409 (C) STRANDEDNESS: single
410 (D) TOPOLOGY: linear
411

412 (ii) MOLECULE TYPE: cDNA
413

415
416 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
417

418 AATTCCATGGG TAGTGTGTGT CCC

23

419 (2) INFORMATION FOR SEQ ID NO:10:
420

422 (i) SEQUENCE CHARACTERISTICS:
423 (A) LENGTH: 23 base pairs
424 (B) TYPE: nucleic acid

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425 (C) STRANDEDNESS: single
426 (D) TOPOLOGY: linear

427
428 (ii) MOLECULE TYPE: cDNA
429

430
431
432 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
433

434 GTACCTATCA CACACAGGGG TTC

23

435
436 (2) INFORMATION FOR SEQ ID NO:11:

437
438 (i) SEQUENCE CHARACTERISTICS:
439 (A) LENGTH: 22 amino acids
440 (B) TYPE: amino acid
441 (C) STRANDEDNESS: single
442 (D) TOPOLOGY: linear

443
444 (ii) MOLECULE TYPE: peptide
445

446
447 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
448

449 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
450 1 5 10 15

451
452 Arg Leu Arg Glu Tyr Tyr
453 20

454
455 (2) INFORMATION FOR SEQ ID NO:12:

456
457 (i) SEQUENCE CHARACTERISTICS:
458 (A) LENGTH: 7 amino acids
459 (B) TYPE: amino acid
460 (C) STRANDEDNESS: single
461 (D) TOPOLOGY: linear

462
463 (ii) MOLECULE TYPE: cDNA
464

465
466
467 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
468

469 Leu Cys Ala Pro Leu Arg Lys
470 1 5

471
472 (2) INFORMATION FOR SEQ ID NO:13:

473
474 (i) SEQUENCE CHARACTERISTICS:
475 (A) LENGTH: 9 amino acids
476 (B) TYPE: amino acid
477 (C) STRANDEDNESS: single

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478 (D) TOPOLOGY: linear
479
480 (ii) MOLECULE TYPE: peptide
481
482
483
484 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
485
486 Cys Arg Pro Gly Phe Gly Val Ala Arg
487 1 5
488
489 (2) INFORMATION FOR SEQ ID NO:14:
490
491 (i) SEQUENCE CHARACTERISTICS:
492 (A) LENGTH: 11 amino acids
493 (B) TYPE: amino acid
494 (C) STRANDEDNESS: single
495 (D) TOPOLOGY: linear
496
497 (ii) MOLECULE TYPE: peptide
498
499
500 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
501
502 Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
503 1 5 10
504
505 (2) INFORMATION FOR SEQ ID NO:15:
506
507 (i) SEQUENCE CHARACTERISTICS:
508 (A) LENGTH: 12 amino acids
509 (B) TYPE: amino acid
510 (C) STRANDEDNESS: single
511 (D) TOPOLOGY: linear
512
513 (ii) MOLECULE TYPE: peptide
514
515
516
517 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
518
519 Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser
520 1 5 10
521
522 (2) INFORMATION FOR SEQ ID NO:16:
523
524 (i) SEQUENCE CHARACTERISTICS:
525 (A) LENGTH: 8 amino acids
526 (B) TYPE: amino acid
527 (C) STRANDEDNESS: single
528 (D) TOPOLOGY: linear
529
530 (ii) MOLECULE TYPE: peptide

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531
532
533
534 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
535
536 Ser Cys Gly Pro Ser Tyr Pro Asp
537 1 5
538

539 (2) INFORMATION FOR SEQ ID NO:17:
540

541 (i) SEQUENCE CHARACTERISTICS:
542 (A) LENGTH: 13 amino acids
543 (B) TYPE: amino acid
544 (C) STRANDEDNESS: single
545 (D) TOPOLOGY: linear
546

547 (ii) MOLECULE TYPE: peptide
548
549

550 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
551

552 Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
553 1 5 10
554

555 (2) INFORMATION FOR SEQ ID NO:18:
556

557 (i) SEQUENCE CHARACTERISTICS:
558 (A) LENGTH: 13 amino acids
559 (B) TYPE: amino acid
560 (C) STRANDEDNESS: single
561 (D) TOPOLOGY: linear
562

563 (ii) MOLECULE TYPE: peptide
564
565
566

567 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
568

569 Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
570 1 5 10
571

572 (2) INFORMATION FOR SEQ ID NO:19:
573

574 (i) SEQUENCE CHARACTERISTICS:
575 (A) LENGTH: 9 amino acids
576 (B) TYPE: amino acid
577 (C) STRANDEDNESS: single
578 (D) TOPOLOGY: linear
579

580 (ii) MOLECULE TYPE: peptide
581
582
583

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584 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

585
586 Pro Gly Trp Tyr Cys Ala Leu Ser Lys
587 1 5
588

589 (2) INFORMATION FOR SEQ ID NO:20:

590
591 (i) SEQUENCE CHARACTERISTICS:
592 (A) LENGTH: 17 amino acids
593 (B) TYPE: amino acid
594 (C) STRANDEDNESS: single
595 (D) TOPOLOGY: linear
596

597 (ii) MOLECULE TYPE: peptide
598

599
600 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

601
602 Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys
603 1 5 10 15
604

605 Arg
606

607
608 (2) INFORMATION FOR SEQ ID NO:21:

609
610 (i) SEQUENCE CHARACTERISTICS:
611 (A) LENGTH: 15 amino acids
612 (B) TYPE: amino acid
613 (C) STRANDEDNESS: single
614 (D) TOPOLOGY: linear
615

616 (ii) MOLECULE TYPE: peptide
617

618
619 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

620
621 Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
622 1 5 10 15
623

624
625 (2) INFORMATION FOR SEQ ID NO:22:

626
627 (i) SEQUENCE CHARACTERISTICS:
628 (A) LENGTH: 9 amino acids
629 (B) TYPE: amino acid
630 (C) STRANDEDNESS: single
631 (D) TOPOLOGY: linear
632

633 (ii) MOLECULE TYPE: peptide
634

635

636

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637 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

638
639 Cys Arg Pro Gly Phe Gly Val Ala Arg
640 1 5

641
642 (2) INFORMATION FOR SEQ ID NO:23:

643
644 (i) SEQUENCE CHARACTERISTICS:
645 (A) LENGTH: 13 amino acids
646 (B) TYPE: amino acid
647 (C) STRANDEDNESS: single
648 (D) TOPOLOGY: linear

649
650 (ii) MOLECULE TYPE: peptide

651
652
653

654 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

655
656 Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser
657 1 5 10

658
659 (2) INFORMATION FOR SEQ ID NO:24:

660
661 (i) SEQUENCE CHARACTERISTICS:
662 (A) LENGTH: 20 amino acids
663 (B) TYPE: amino acid
664 (C) STRANDEDNESS: single
665 (D) TOPOLOGY: linear

666
667 (ii) MOLECULE TYPE: peptide

668
669
670

671 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

672
673 Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly
674 1 5 10 15

675
676 Thr Phe Ser Lys
677 20

678
679 (2) INFORMATION FOR SEQ ID NO:25:

680
681 (i) SEQUENCE CHARACTERISTICS:
682 (A) LENGTH: 20 amino acids
683 (B) TYPE: amino acid
684 (C) STRANDEDNESS: single
685 (D) TOPOLOGY: linear

686
687 (ii) MOLECULE TYPE: peptide

688
689

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690 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
691
692 Cys Arg Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp
693 1 5 10 15
694
695 Val Val Cys Lys
696 20
697

698 (2) INFORMATION FOR SEQ ID NO:26:
699

700 (i) SEQUENCE CHARACTERISTICS:
701 (A) LENGTH: 18 amino acids
702 (B) TYPE: amino acid
703 (C) STRANDEDNESS: single
704 (D) TOPOLOGY: linear
705

706 (ii) MOLECULE TYPE: peptide
707
708
709

710 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
711

712 Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln
713 1 5 10 15
714
715 Leu Trp
716

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TIME: 06:31:53

LINE ERROR

ORIGINAL TEXT

33 Wrong application Serial Number

(A) APPLICATION NUMBER: US 07/625668



PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/625,668A

DATE: 05/08/92
TIME: 06:31:53

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/625,668A

DATE: 05/08/92

TIME: 06:31:53

LINE ORIGINAL TEXT

CORRECTED TEXT